

Figure 1A
Neutrokinine-α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGACGCAGGAC 60

61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120

121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
1 M D D S T E R E Q S R L 12

181 TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC 240
13 T S C L K K R E E M K L K E C V S I L P 32
CD-I

241 CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAGCTGCTGGCTGCAACCT 300
33 R K E S P S V R S S K D G K L L A A T L 52
CD-I

301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTTACCAGGTGGCCGCC 360
53 L L A L L S C C L T V V S F Y Q V A A L 72

361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
73 Q G D L A S L R A E L Q G H H A E K L P 92
CD-II

421 CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC 480
93 A G A G A P K A G L E E A P A V T A G L 112
CD-III

481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
113 K I F E P P A P G E G N S S Q N S R N K 132

541 AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
133 R A V Q G P E E T V T Q D C L Q L I A D 152
CD-IV

601 ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT 660
153 S E T P T I Q K G S Y T F V P W L L S F 172
CD-V

661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCRAAGAAACTGGTT 720
173 K R G S A L E E K E N K I L V K E T G Y 192
CD-V CD-VI

721 ACTTTTTTATATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAA 780
193 F F I Y G O V L Y T D K T Y A M G H L I 212
CD-VI CD-VII

781 TTCAGAGGAAGAAGGTCCATGTCTTTGGGATGAATGAGTCTGGTGAAGTTGTTTCGAT 840
213 Q R K K V H V F G D E L S L V T L F R C 232
CD-VII CD-VIII

841 GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAA 900
233 I O N M P E T L P N N S C Y S A G I A K 252
CD-VIII CD-IX

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[illegible]

901	AACTGGAAGAAGGAGATGAACCTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L O L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTACATTTTTTGGTGCATTGAAACTGCCTGTGACCTACTTACACCATGT	1020
273	D G D V <u>T F F G A L K L</u> L	285
	CD-XI	
1021	CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAAA 1100	

1081 CCAAAAAAAAAAAAAAAAAAAAAA 1100

FIGURE 2A

	10	20	30	
1	M S T E S M I R D V E L	- - - - -	- - - - - A E E A	TNFalpha
1	M - - - - -	- - - - -	- - - - - T P P E R L	TNFbeta
1	M G A - - - - -	- - - - -	- - - - -	LTbeta
1	M Q Q P F N Y P Y P Q I Y W - V D S S A S S P W A P P G T V			FasLigand
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokin alpha
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokin alphaSV
	40	50	60	
17	L P K K T G G P Q - - G S R R - - - - -			TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - - L G L E G R G G - - - - -			LTbeta
30	L P C P T S V P R R P G Q R R P P P P P P P P L P P P P P			FasLigand
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokin alpha
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokin alphaSV
	70	80	90	
30	- - - - -	- - - - - C L F L S L F S		TNFalpha
9	- - - - - L P R V R G T T L H L L L L G L L L V L L P			TNFbeta
12	- - - - - R L Q G R G S L L L A V A G A T S L V T			LTbeta
30	P P P L P P L P L P P L K K R G N H S T G L C L L V M F F M			FasLigand
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alpha
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alphaSV
	100	110	120	
38	F L - - I V A G A T T L F C L L H F G V I G P Q R E E F P R			TNFalpha
31	G A Q G L P G V G L - - - - -	- - - - -	- - - - -	TNFbeta
32	L L L A V P I T V L A V L A L V P Q D Q G G L V T E T A D P			LTbeta
90	V L V A L V G L G L G M F Q L F H L Q K E L A E L R E S T S			FasLigand
38	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alpha
38	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alphaSV
	130	140	150	
66	D L S L I S - P L A - Q A V R S S S R T P S D - - - K P V A			TNFalpha
41	- - - T P S - A A Q - T A R Q H P K M H L A H S T L K P A A			TNFbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S P G L P A A			LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A			FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T Q D C L			Neutrokin alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T - - - - -			Neutrokin alphaSV
	160	170	180	
91	H V V A N P Q A E G - Q - - - - - L Q W L N R R A N A L L			TNFalpha
66	H L I G D P S K Q N - S - - - - - L L W R A N T D R A F L			TNFbeta
91	H L I G A P L K - G Q G - - - - - L G W E T T K E Q A F L			LTbeta
148	H L T G K S N S R S M P - - - - - L E W E D T Y G I V L L			FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P W L - - - - L S F K			Neutrokin alpha
142	- - - - - - - - - - G S Y T F V P W L - - - - L S F K			Neutrokin alphaSV

FIGURE 2B

	190	200	210	
114	A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G			TNFalpha
89	Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G			TNFbeta
114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G			LTbeta
172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G			FasLigand
174	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			Neutrokin alpha
155	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D			Neutrokin alphaSV
	220	230	240	
143	Q G C P - - - - - S T H V L L T H T I S R I A V S Y Q T K			TNFalpha
118	K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H			TNFbeta
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G			LTbeta
200	Q S C N - - - - - N L P L S H K V Y M R N S K Y P Q D			FasLigand
204	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -			Neutrokin alpha
185	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -			Neutrokin alphaSV
	250	260	270	
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E			TNFalpha
146	V P - - L L S S Q K M V Y P - - - - - G L Q E P W L H			TNFbeta
174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T			LTbeta
222	L V - - M M E G K M M S Y C - - - - - T T G Q M W A R			FasLigand
226	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokin alpha
207	L V T L F R C I Q N M P E T L P N - - - - - N			Neutrokin alphaSV
	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E			TNFalpha
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P			TNFbeta
204	S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R			LTbeta
242	S S Y L G A V F N L T S A D H L Y V N V S E L S L V N F E E			FasLigand
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokin alpha
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D			Neutrokin alphaSV
	310			
223	S G Q V Y F G I I A L			TNFalpha
196	S - T V F F G A F A L			TNFbeta
234	- G K T F F G A V M V G			LTbeta
272	S - Q T F F G L Y K L			FasLigand
274	G D V T F F G A L K L L			Neutrokin alpha
255	G D V T F F G A L K L L			Neutrokin alphaSV

Figure 3
Neutrokinine- α

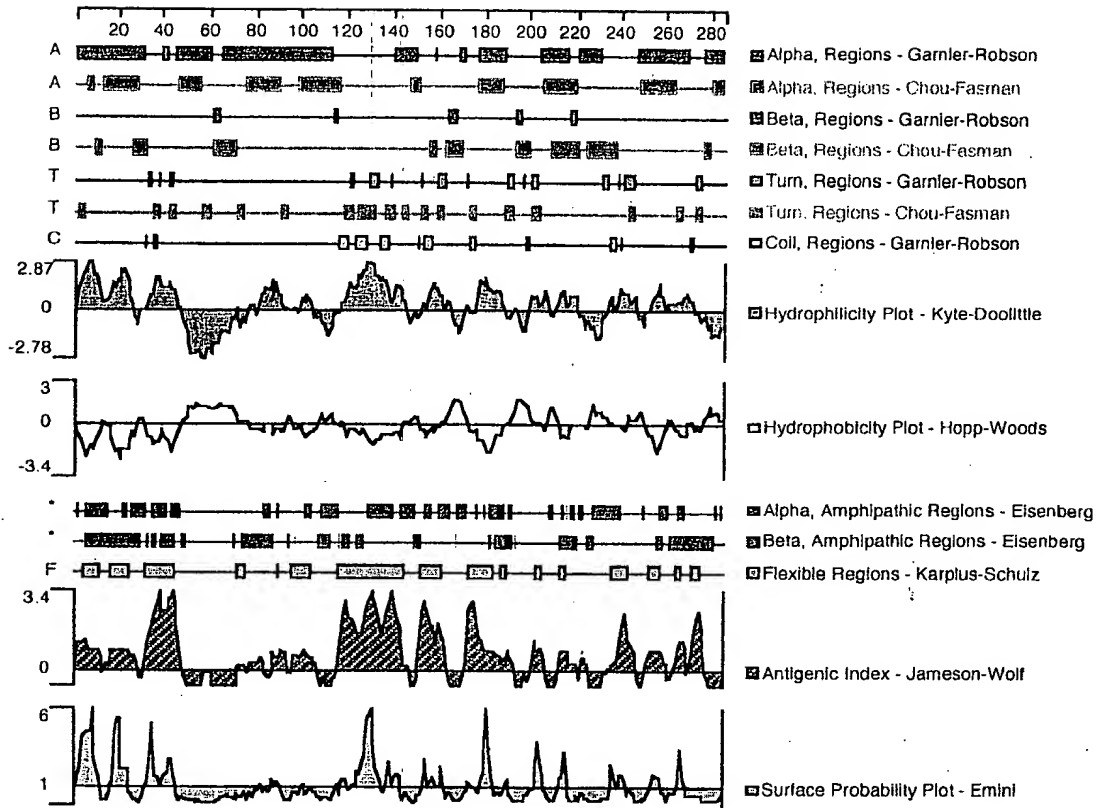


FIGURE 4 A

	1		50
HSOAD55RA	GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA	
HNEDU15X	...AAATTCA	GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA	
HSLAH84R	.AATTCGGCA	NAGNAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT	
HLTBM08R	AATTCGGCAC	GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCAACGCG	
	51		100
HSOAD55R	GTGCACGCAG	GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC	
HNEDU15X	GTGCACGCAG	GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC	
HSLAH84R	ATACTGATAA	GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC	
HLTBM08R	GGACTGAAAA	TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA	
	101		150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA	
HNEDU15X	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA	
HSLAH84R	CATGTCTTTG	GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA	
HLTBM08R	GAACAGCAGA	AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC	
	151		200
HSOAD55R	TATGGATGAC	TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA	
HNEDU15X	TATGGATGAC	TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA	
HSLAH84R	AAATATGCCT	GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG	
HLTBM08R	AAGACTGCTT	GCAACTGNNT GCAGACAGTG AAACACCAAC TATACAAAAA	
	201		250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG	
HNEDU15X	AGAAAAGAGA	AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG	
HSLAH84R	CAAACTGGN	AGGAAGGA... .GATGAAC TCCAACCTGC AATACCAGGG	
HLTBM08R	GGCTCCCTTC	TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG	
	251		300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC GATCCTCCAA AGACGGAAAAG CTGCTGGCTG	
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC GATCCTCCAA AGACGGAAAAG CTGCTGGCTG	
HSLAH84R	GAAAATGCAC	AATTATCACT GGGATGGAGA TGTTACATT TTTTGGGTGC	
HLTBM08R	TCTGGAAACA	TTTTGCCAAA CTCTTCAGAT ACTCTTNCT CTCTGGGAAT	
	301		350
HSOAD55R	CAACCTTGNT	GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTNTT.	
HNEDU15X	CAACCTTGCT	GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC	
HSLAH84R	CATTGAACT	GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC	
HLTBM08R	CAAAGGAAAA	TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT	
	351		400
HSOAD55R	
HNEDU15X	TACCAGGTGG	CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT	
HSLAH84R	CTNCCTNTTC	TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA	
HLTBM08R	AAGTTTTTAA	AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC	

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FIGURE 4B

	401				450
HSOAD55R
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC	AGGAGCAGGA	GCCCCCAAGG
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN	GNNANANGNG	GGGNGTTNN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC	AGGTTTNTAT	ANCTGGTAGG
	451				500
HSOAD55R
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG	CGGGACTGAA	AATCTTTGAA
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN	GGGNNNGTA	AAAATGGGGC
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG	NCNNTCTTTT	GGGNTGA...
	501				550
HSOAD55R
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT	CAGAACAGCA	GAAATAAGCG
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551				600
HSOAD55R
HNEDU15X	TGCCGTTTCA	GGTCCAGAAG	AAACAGTCAC	TCAAGACTGC	TTGCAACTGA
HSLAH84R
HLTBM08R
	601				650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA	AAGGATCTTA	CACATTTGTT
HSLAH84R
HLTBM08R
	651				700
HSOAD55R
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT	GCCCTAGAAG	AAAAAGAGAA
HSLAH84R
HLTBM08R
	701				750
HSOAD55R
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT	TTTTATATAT	GGTCAGGTTT
HSLAH84R
HLTBM08R
	751				800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC	ATCTAATTCA	GAGGAAGAAG
HSLAH84R
HLTBM08R

000000-000000

Figure 5A
Neutrokin- α SV

1 ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA 60
1 M D D S T E R E Q S R L T S C L K K R E 20

61 GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCCCTCTGTCCGA 120
21 E M K L K E C V S I L P R K E S P S V R 40
CD-I

121 TCCTCCAAAGACGGAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC 180
41 S S K D G K L L A A T L L L A L L S C C 60
CD-I

181 CTCACGGTGGTGTCTTTTCTACAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240
61 L T V V S F Y Q V A A L O G D L A S L R 80
CD-II

241 GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC 300
81 A E L Q G H H A E K L P A G A G A P K A 100
CD-II CD-III

301 GGCCTGGAGGAAGCTCCAGCTGTACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA 360
101 G L E E A P A V T A G L K I F E P P A P 120
CD-III

361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAAGGTCCAGAAGAA 420
121 G E G N S S Q N S R N K R A V Q G P E E 140

421 ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA 480
141 T G S Y T F V P W L L S F K R G S A L E 160
CD-IV

481 GAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTATATATGGTCAGGTT 540
161 E K E N K I L V K E T G Y F F I Y G O V 180
CD-IV CD-V

541 TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGTCCATGTC 600
181 L Y T D K T Y A M G H L I O R K K V H V 200
CD-VI CD-VII

601 TTTGGGGATGAATTGAGTCTGGTGACTTTTGTTCGATGTATTCAAAATATGCCTGAAACA 660
201 F G D E L S L V T L F R C I O N M P E T 220
CD-VIII CD-VIII

661 CTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC 720
221 L P N N S C Y S A G I A K L E E G D E L 240
CD-IX CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780
241 Q L A I P R E N A Q I S L D G D V T F F 260
CD-X CD-XI

781 GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCTCCCTTTC 840
261 G A L K L L 266
CD-XI

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[illegible]

901 AAA 903

Figure 6
Neutrokinine- α SV

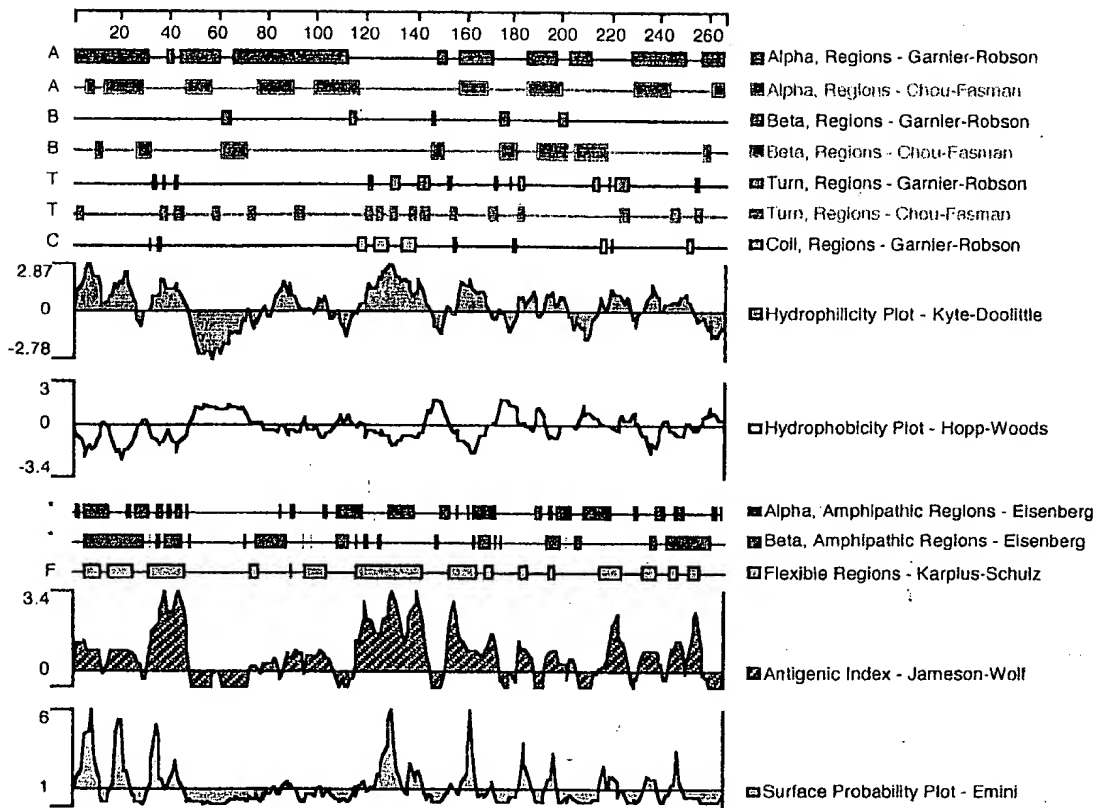


Figure 7

a.

leutokine-

alpha MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKDGLLAATLLALLSCCLTVVSFYQVAALQGD LASLRAE 82

LQGHHA EKLPAGAGAPKAGLEEAPAVTAGL KIFEPPAPGEG 123

NSSQNSRNKRAVQGP EETVT QDC O L I A B S E P T I Q K G S Y 164
 April H S V H V P I N A S K - D D S D V 134
 TNF K P V A H V V N P Q A E G Q - - - - - 102
 LT α K P A A H L L G D P S K Q N S - - - - - 77

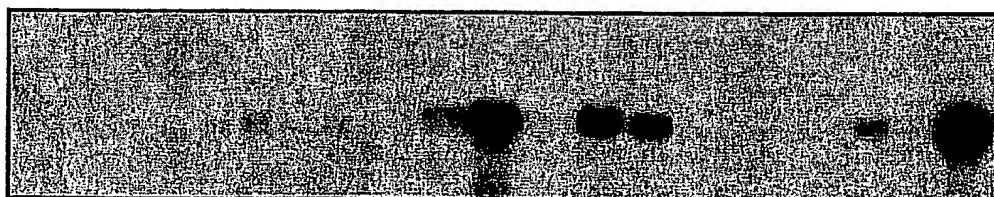
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 E V M W Q P A - - - - F R R G R G I Q A Q G Y G V R I Q D A G V V L L Y S Q V L 170
 - L Q W L N R R A N A L L A N G V E T R D - - N Q I V V P S E G L V L L Y S Q V L 139
 - L L W R A N T D R A F Q D C F S E S N - - N S L L V E T S C I Y F V Y S Q V V 114

Y T D K L V - - - - A M G S L I Q R K K V H V G D E L S L V T T F R C L O N M P 237
 E Q D V T F - - - - M G Q V V S R E - - - - G G R Q E T T F R C I R S M P 201
 K G Q G C P - - - - S T V L E T H T I S R I A V S N Q T K V N L L S A I K S P 176
 S G A A V S P K A T S S P L Y T A H E V Q L H S S S V P F H V P L L S S O R M V 155

E - - T L S - - - - - N N S C Y S A G I A K L E E G D E F Q L A T P R E N A 268
 S H P D R A - - - - - Y N S C Y S A G V F H H H O G D I F V I L P R A R A 234
 C Q R E T P E G A E A K P W K E P I N L G G V F O I K G D R L S A E N R P D Y 217
 Y P - - - - - G L Q E P W L H S M H G A A E O I T O G D Q L S T H T D G I P H 190

Q I S D G D V D F F G A L K L L 285
 K L N S H G H L G F V K L 250
 D F A E S G Q V Y F G I A E 233
 V L S - S T V F L G A F A 205

b.



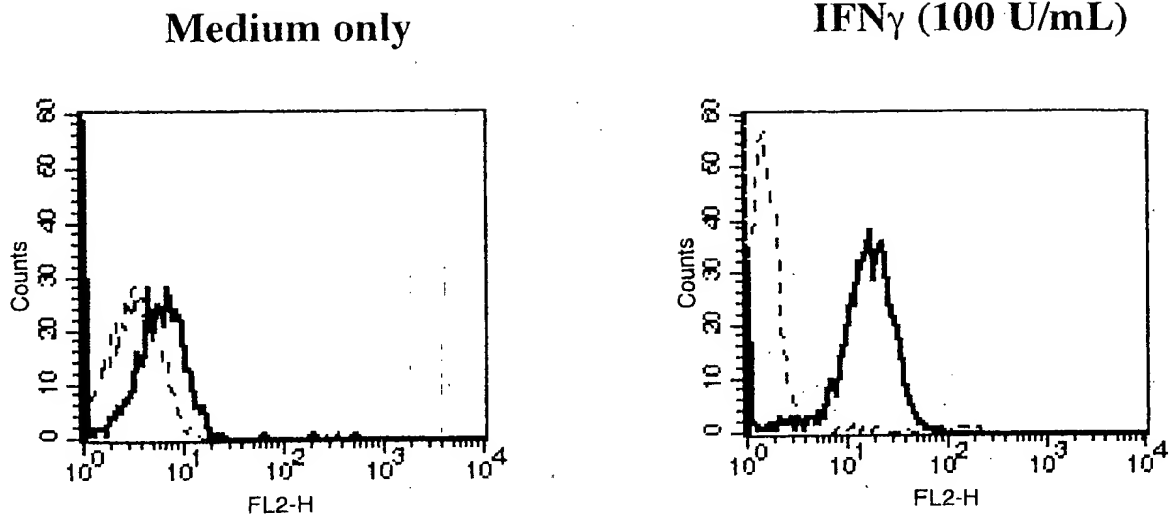
- 4.4 kb

- 2.4 kb

HL-60
 HeLa
 K-562
 MOLT-4
 Raji
 SW480
 Spleen
 Lymph Node
 Thymus
 PBL
 Bone Marrow
 Fetal liver
 Heart
 Brain
 Placenta
 Lung
 Liver
 S. Muscle
 Kidney
 Pancreas

Figure 8

a.



b.

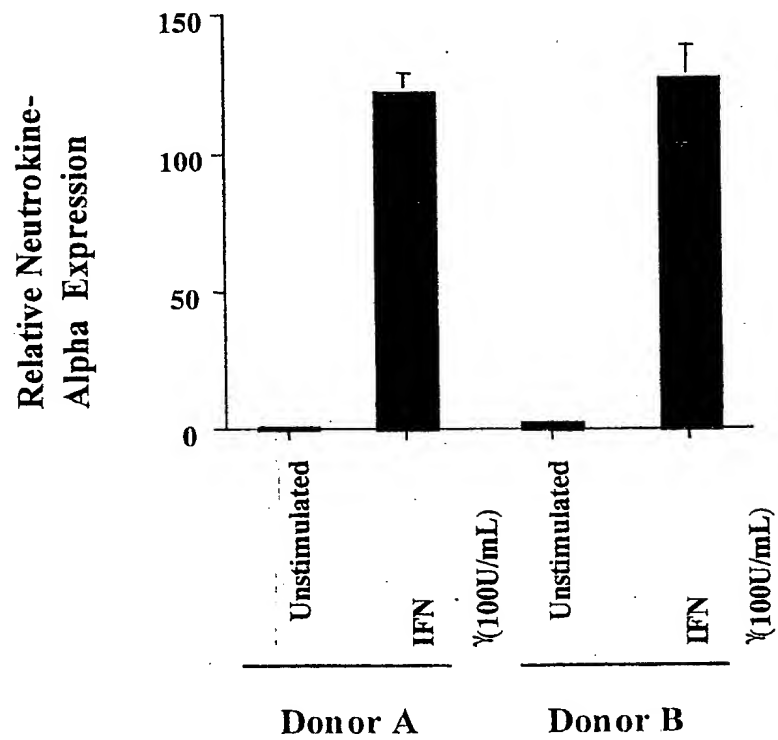
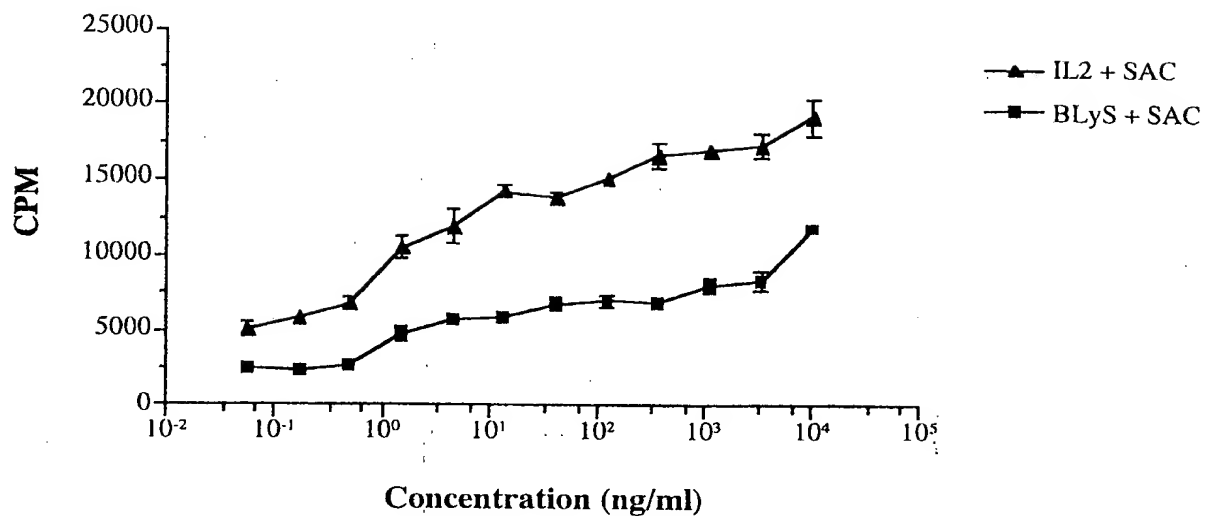


Figure 9

a.



b.

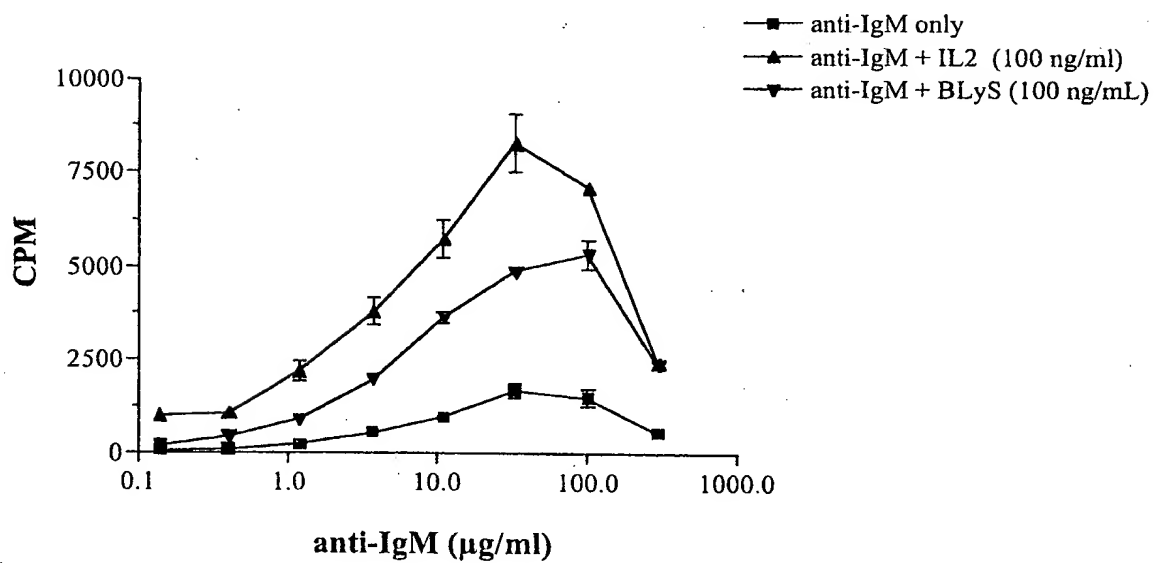
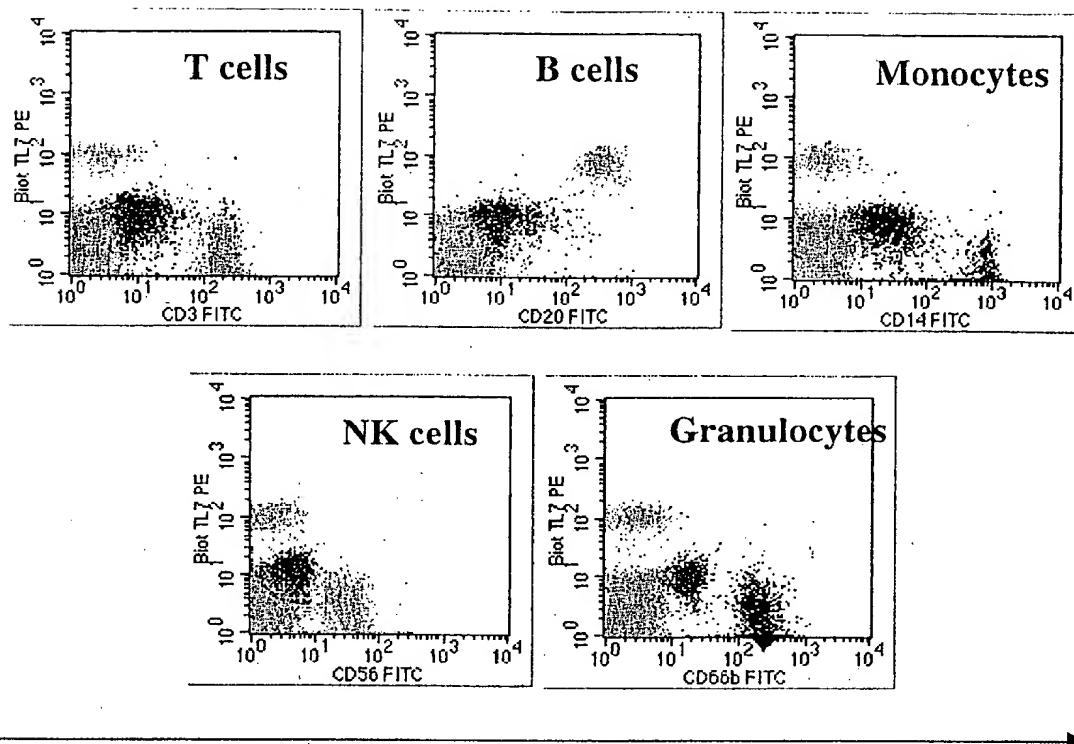


Figure 10

a.

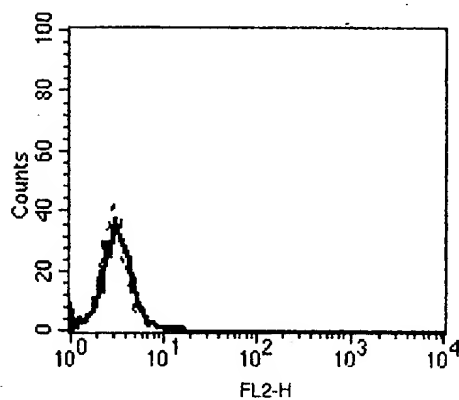
**Biotinylated Neutrophil-
alpha binding**



Hematopoietic lineage markers

b.

U-937



IM-9

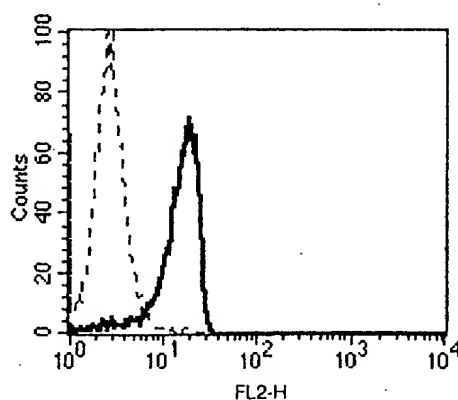


Figure 11

